However, BW was associated ($P<0.05$) with differences in all EBV except those for fiber diameter and staple length. Ewes with single litters had higher CS during L than ewes with larger litters ($P<0.05$). Heritability estimates for CS were 0.10, 0.15 and 0.16 for G, L and P, respectively. Permanent environment effects were not significant ($P<0.10$). The genetic relationships that exist between performance potential, BW, and CS may be useful in estimating adult ewe performance.

Key Words: Sheep, Heritability, Body Weight

134 Genomic organization and six exonic polymorphisms of the pig SLC11A1 gene. W. Zhen-Fang*, L. Wen-Hua, Z. Xi-Chuan, and Y. Guan-FU, *South China Agricultural University*, *Guangzhou, Guangdong, China*.

SLC11A1 gene plays a crucial role in animal disease resistance to several intracellular pathogens such as Mycobacterium, Leishmania and Salmonella. In this study, PCR amplification and sequencing were performed to obtain the genomic organization of pig SLC11A1 gene by comparative genomic analysis. Results showed that pig SLC11A1 gene consists of 15 exons and 14 introns, which is consistent with the mouse, human SLC11A1 gene. All of the introns sequence acquired have been submitted to GenBank and assigned the accession numbers AY368468, AY368469, AY368470, AY368471, AY368472, AY368473, AY368474, AY368475, AY556536, AY368476, AY368477, AY368478, AY368479, AY368480,respectively. The full gene spans 12,267 bp. Mutational analysis was performed on the exonic regions. Six single nucleotide polymorphisms (SNPs) are identified, two are nonsynonymous, three are synonymous, and one is in 3'UTR region. The SNP G80C in exon2 results in the change Asp6 to His6; and G587A in exon6 results in the change of Val175 to Ile175. The availability of the fine genomic organization of the pig SLC11A1 gene and the identification of polymorphisms will facilitate the evaluation of its functional role in several diseases resistance or susceptibility.

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Key Words: Pig SLC11A1 Gene, Genomic Organization, Single Nucleotide Polymorphism

135 Detection of imprinted quantitative trait loci for growth, carcass, and meat quality traits in swine. N. Vukasinovic*[1], A. Clutter[1], F. Du[1], M. Lohuis[1], L. Messer[1], J. Bennewitz[2], N. Borchers[2], N. Reinsch[2], G. Otto[2], K. Sanders[2], and E. Kalm[2], [1]*Animal AG, Monsanto*, *St. Louis, MO*, [2]*University of Kiel*, *Kiel, Germany*.

Detection of imprinted quantitative trait loci (QTL) affecting growth, carcass, and meat quality was conducted in an F2 population created by crossing Pietrain boars with Large White x Landrace hybrid sows. 1014 F2 animals, their parents and grandparents were genotyped for 27 microsatellite markers on chromosomes 2, 6, and 7. Phenotypes on 31 growth, carcass, and meat quality traits were available. Imprinting analysis was performed using the following methods: (1) the imprinting effect was fitted along with additive and dominance effect; imprinting was inferred if the model with imprinting was significantly better than the null model without QTL and the Mendelian model without imprinting (Knott et al., Genetics 149, 1998); (2) maternal and paternal allele effects were fitted separately; imprinting was declared if the full model (with paternal, maternal, and dominance effect) was significantly better than the model with only one parental component and no dominance (De Koning et al., JAS 79, 2001); and (3) Mendelian, full, paternal, and maternal models were evaluated using a decision tree to determine presence and mode of inheritance of QTL (Thomsen et al., WCGALP Proceedings, 2002). All three methods detected several QTL for growth, fatness, and meat color and conductivity on SSC2, most of which were (paternally) imprinted. With method (3), QTL for abdominal fat, loin eye area, and meat color were partially imprinted. Methods (1) and (2) did not infer imprinting for QTL affecting backfat, meat color, and meat reflectance. No QTL was detected on SSC6, except for a paternally imprinted QTL for birth weight detected by method (3). On SSC7, all three methods detected Mendelian QTL affecting carcass length and backfat; in addition, method (3) detected partially imprinted QTL for ham weight and percentage, and loin eye area. These results confirmed previous findings of paternally imprinted QTL for growth and fatness on SSC2 and provided evidence of additional imprinted QTL.

Key Words: Imprinting, QTL Mapping, Swine

136 Discrete time survival analysis of longevity in a colony of dog guides. J. Cole*[1], B. Southey[2], D. Franke[3], and E. Leighton[4], [1]*Animal Improvement Programs Laboratory, Agricultural Research Service, USDA*, *Beltsville, MD*, [2]*University of Illinois*, *Urbana*, [3]*Louisiana State University*, *Baton Rouge*, [4]*Seeing Eye, Inc.*, *Morristown, NJ*.

Working life for 1,177 German Shepherd (GS) and 1,724 Labrador Retriever (LR) dogs that worked as guides for the blind was studied using discrete time survival analysis. Total years worked after graduation, total months worked after graduation, months worked between graduation and 18 mo (EWL), and months worked beyond 18 mo (LWL) were analyzed using complementary log-log animal and maternal effects models. Animals working 10 or more years were combined in a single group. Censoring rates were 91.76% (44.87%) and 94.90% (48.90%) for EWL (LWL) in GS and LR, respectively. Explanatory variables were duration of time interval (months or years), contemporary group, sex, and inbreeding coefficient. Estimates of explanatory variables obtained within the same period across models and different time intervals were similar. No sex differences were observed and the hazard of culling increased with increasing inbreeding coefficient. Maternal effects were small and non-significant in both breeds for all traits. Heritability estimates ranged from 0.05 to 0.12 in GS and 0.04 to 0.15 in LR and were lowest for later working life, intermediate for total working life in months or years, and highest for early working life. These estimates were higher than the previously reported estimates of 0.03 (0.02) and 0.05 (0.03) for EWL (LWL) in GS and LR, respectively, that were obtained with a Weibull sire model. Pearson's product-moment correlations among sire estimated breeding values for EWL and LWL were 0.92 and 0.83 for GS and LR, respectively, suggesting that EWL and LWL are biologically different traits. These results suggest that there is sufficient genetic variability that can be exploited to genetically improve working life.

Key Words: Dog, Heritability, Longevity

Breeding and Genetics: Statistical Methods II

137 Bayesian inferences on major genes affecting polygenic binary traits: comparison of models and application to osteochondral diseases in pigs. H. N. Kadarmideen*[1] and L. L. G. Janss[2], [1]*Swiss Federal Institute of Technology*, *Zurich, Switzerland*, [2]*Wageningen University and Research Centre*, *Lelystad, The Netherlands*.

The main objective of this study was to develop and apply Bayesian segregation analysis (BSA) method to detect major genes for binary polygenic traits and to investigate different BSA models. In order to apply developed methods, osteochondral (OC) diseases in pigs (as scores or binary data) were modeled by a mixture inheritance linear model (MILM) and threshold model (MITM) and analyzed by Bayesian-Gibbs sampling algorithms. Data, on 1163 pigs with OC (pedigree with 2891 animals), were from company, SUISAG. Both MILM and MITM included systematic environmental effects, animals polygenic effects and a major gene effect with *Mendelian* transmission probabilities. Results showed familial transmission and evidence for segregating major gene with

significant major gene variances; range of MILM parameters was, additive effect = 0.466 to 0.587, dominance effects = -0.587 to -0.468, additive major gene variances = 0.011 to 0. 0.162, dominance major gene variances = 0.016 to 0.058 and disease allele frequencies = 0.45 to 0.83. Magnitudes of parameters were higher for MITM than MILM, as expected. BSA based on *individual animal model* analysis on very low incidence (2.0-4.0%) data caused poor mixing and convergence of Gibbs chains, mostly with MILM than MITM. Further, polygenic variances were outside bounds or overestimated. A variant of BSA, *the informative prior model*, with a *prior* and weight for polygenic variance provided significant improvements. Another variant, the *reduced animal model* was implemented to sample *transmitting abilities* of only parents (major gene probabilities were still sampled for each animal); results showed improvements with larger family sizes. Results from this study provided better insights into BSA for binary traits which would be useful across many animal species as well as humans.

138 Statistical analysis of relative quantification of gene expression using real time RT-PCR data. J. Steibel*, R. Poletto, and G. Rosa, *Michigan State University*, *East Lansing*.

The objective of this work is to assess the use of linear models for the analysis of RQ-RT-PCR experiments. Reverse Transcription (RT) followed by the polymerase chain reaction (PCR) is the most accurate and sensitive method to quantify relative or absolute levels of mRNA transcription of selected genes. The relative quantification (RQ) is based on the comparative expression (fold change) of a target gene under two conditions, avoiding the production of costly standard material necessary for absolute quantification. Complex hypotheses are usually tested in gene expression studies using factorial experimental structures and hierarchical levels of replication, which require suitable analysis. In the literature, however, the statistical procedures used for RQ-RT-PCR data either ignore the distinction between technical and biological variability or are restricted to simple cases where only two experimental groups are considered. As a consequence, estimated fold changes and associated p-values are generally invalid. Here we discuss linear models for the analysis of RT-PCR data, under two alternative specifications: a) models assuming normality of the mRNA concentration, and b) models assuming normality in the log scale. Variable definition, hypothesis testing and fold-change estimation are presented for each case. Normality tests are used to determine the most appropriate scale and analysis approach. The implementation of the different procedures is illustrated using data from an experiment on gene expression in brain of piglets subjected to social isolation and weaning. The experiment involves a 2´2´2 factorial structure in a split-plot design. The results show that, as opposed to the traditional methods, a linear model fitted to the log scale can be used to test any linear hypothesis about differential expression and to obtain point estimates and confidence intervals of the fold change for any pair-wise comparison of RQ-RT-PCR data. Moreover, this model allows the inclusion of genetic and environmental effects (such as litter) and leads to valid inferences by appropriately modeling the different levels of replication.

Key Words: RT-PCR, Relative Quantification, Statistical Analysis

139 Exploiting non-additive effects of imprinted QTL in marker-assisted selection by genetic algorithm. Y. Li*[1], H. N. Kadarmideen[1], J. H. J. van der Werf[2], and B. P. Kinghorn[2], [1]*Swiss Federal Institute of Technology, ETH-Zentrum*, *Zurich, Switzerland*, [2]*University of New England*, *Armidale, Australia*.

Incorporation of quantitative trait locus (QTL) in conventional breeding program is a focus in modern animal breeding. Imprinted QTL has been detected in some animal species. The objective of this study was to investigate superiority of mate selection with an imprinted QTL over index selection in a model including polygenic effects and QTL effect in overlapping generations. Benefit from mate selection was optimized by using a genetic algorithm according to total benefit (including those from polygenes and QTL) from progeny generation while index selection was conducted with an index consisting of sum of BLUP (best linear unbiased prediction) estimated breeding values of polygenes and breeding value of the QTL. Polygenic effects were assumed to follow an infinitesimal model with 0.3 of heritability. A maternal imprinted QTL was assumed with inactive allele inherited from female parent. The additive effect of the allele inherited from male parent was 1.0 of the additive standard deviation of polygenes. A population with 200 dams and 20 sires at 4 age groups in overlapping generations were used, 50 dams and 5 sires being selected each year. The number of progeny per family was 2. Initial frequency of the favorable allele of the QTL was 0.1. Mate selection produced about 40% extra benefit over index selection was achieved. When the QTL is maternally imprinted, selection pressure on QTL was put on the male parents because the allele inherited from the female parents was silent, therefore, genotype of the QTL was optimized in selection of sires and in mating allocation in the mate selection.

Key Words: Imprinted QTL, Marker-Assisted Selection, Genetic Algorithm

140 Experimental design for estimation of breed, heterosis, and QTL effects in cattle. R. M. Thallman*, L. V. Cundiff, and G. L. Bennett, *USDA-ARS-USMARC*, *Clay Center, NE*.

Generation of data to provide ties between breeds and breed-specific heterosis estimates for support of multibreed national cattle evaluation has become a primary objective of the Germplasm Evaluation Program (GPE) at the U.S. Meat Animal Research Center. Consequently, more emphasis will be placed on continual re-sampling of highly influential purebred sires with high accuracy EPD. A change in design that incorporates the following elements is being considered: Purebred cows and cows 75% or slightly more of their sire breed (SB75) would be bred AI to bulls of a different breed to produce progeny 50% or slightly more of their sire breed (SB50), which would in turn be bred AI to bulls of their sire breed to produce SB75 progeny. Approximately 25% of the cow herd would be purebreds of four breeds, 40% would be SB50, and 35% would be SB75. All AI sired heifers would be retained in the herd for maternal evaluation and (with the exception of some purebred cows) all cows would be AI-sired. Substantially greater information can be generated from the same number of cows by designing the population in such a way that every calf contributes to estimates of both direct and maternal effects. This design would provide a set of powerful resource populations with extensive phenotypes for detection and characterization of QTL. Sampling highly influential sires would ensure that the population segregated most polymorphisms relevant to the U.S. beef industry. Progeny of F_1 cleanup bulls would contribute directly to project objectives by providing large paternal half-sib families with complete carcass phenotypes. Different subsets of the population would be most effective for each of several genomics objectives. Direct and maternal breed-specific heterosis, as well as breed effects and QTL effects, should be estimable under the proposed design using a model accounting for breed contributions and expected heterozygosity. Using the same population for several complementary objectives is the most efficient use of limited resources.

Key Words: Breed Evaluation, Heterosis, QTL

141 Hierarchical Bayesian model for analysis of gene expression data. R. Rekaya* and W. Zhang, *University of Georgia*, *Athens*.

In the last few years several ANOVA based models have been proposed both for spotted cDNA microarray and for oligonucleotide data analysis. Estimating all effects, including gene effects, in a global ANOVA model is computationally challenging due to the large number of parameters to be inferred. Consequently, ANOVA analyses for microarray data are usually implemented in two stages. The first stage consists in modeling global effects affecting the expression levels fellowed by a within gene model that fits the data of each gene separately. Although this approach helps solve the computational challenge, it has two major problems: 1) the residual terms of the first stage model are usually assumed non-correlated. Such assumption is often not true, especially when the gene effects within array are not included in the model 2) the fitted residuals of the first stage are used as dependent variables of the second stage model with-

out consideration of their uncertainty. To overcome these two problems a hierarchical Bayesian model with three stages was proposed where the extra stage was included to account for the potential correlations between expression levels of a gene within the same array. To evaluate the performances of the proposed model, a simulation was conducted. Given the complexity of simulating microarray data, a novel approach was developed. It consisted in using real gene expression data from which only records corresponding to one treatment level (reference treatment level) were kept. Records for each of the other treatment levels were generated by adding a random quantity (difference between the effect of the reference level and the new treatment level for which data is being generated) to the observed expression for the reference treatment level. The performances of the proposed and classical two stage models were evaluated based on their ability in correctly estimating the true differences between treatment levels. In all cases, the proposed approach proved to be superior to the classical two stage model. Such superiority ranged from 10 to 37% depending on the simulation parameters

Key Words: Hierarchical Model, Bayesian, Gene Expression

142 A simulation study for analysis of uncertain binary responses using fuzzy logic classification. R. L. Sapp*, M. L. Spangler, R. Rekaya, and J. K. Bertrand, *The University of Georgia*, *Athens*.

A simulation was carried out to investigate methods of analyzing uncertain binary responses for first insemination success (FIS). A linear mixed model that included herd, year, and month of mating as fixed effects; and unrelated service sire, sire and residual as random effects were used to generate binary data. Binary responses were assigned using the difference between days to calving (DC) and average gestation length (GL). If the difference between DC and average GL was less than or equal to 21 days then FIS = 1, otherwise FIS = 0; in other words, a successful FIS event was defined as conception occurring during the first 21 days of the breeding season. Females deviating from average GL leads to uncertain binary responses. The methods investigated were: 1) threshold model (TM) fitted to certain (no uncertainty) binary data (M1); 2) TM fitted to uncertain binary data ignoring uncertainty (M2); and 3) analysis of uncertain binary data, accounting for uncertainty from day 16 to 26 (M3) or from day 14 to 28 (M4) after introduction of the bull, using a TM with fuzzy logic classification. Three different fuzzy logic functions were utilized to account for uncertain FIS responses. There was virtually no difference between point estimates obtained from M1, M3, and M4 with the true values used in the simulation. When uncertain binary data were analyzed ignoring uncertainty (M2), sire variance and heritability were under estimated by 22 and 24%, respectively. In this study, the mean and standard deviation of GL were used to assess the probability of miscoding of FIS via fuzzy logic classification. There did not appear to be large differences between the intervals (14 to 28 days vs. 16 to 26 days) or fuzzy logic functions (two linear and one non-linear) used to account for uncertainty of FIS. The results of this study suggest that when analyzing binary data with uncertainty, a standard TM could lead to biased inferences. Bias could be avoided using a statistical model that contemplates uncertainty through fuzzy logic classification.

Key Words: Binary Response, Fertility, Fuzzy Logic

143 Dealing with extreme case problem in the analysis of binary responses. W. Zhang*, R. Rekaya, and K. Bertrand, *The University of Georgia*, *Athens*.

Binary responses, such as health and fertility traits, are often included in the routine genetic evaluation of livestock. The latent model postulates a continuous variable (liability) underling the discrete measurement and has been widely used in genetic analysis. When the occurrence rate of one binary outcome (+ or -) is low, observations in some contemporary groups, especially those with small size, can fall into the same category. In this situation, the maximum likelihood estimates of the associated location parameters do not exist theoretically, yielding the so-called "extreme case problem (ECP)". Two novel ad hoc methods for addressing ECP within the framework of a Bayesian approach are proposed: 1) adopting g-priors for the location parameters associated with ECP, 2) inserting a pseudo record for each ECP class with an approximate liability derived from a α% (such as 5%) upper limit of the probability of the unobserved response in ECP classes according to a Poisson model. Both methods are based on the assumption that the effects associated with ECP classes are finite and the large estimates with regular methods are due to abnormality in the likelihood. Thus, the proposed methods tend to restrict the estimates of the location parameters for ECP classes. In other words, the extreme case problem is simplified to a zero-numerator problem, which postulates that an event is conceivably possible but has not yet occurred in the available data. The analyzed data was simulated with a sire model, 8-50% ECP ratio, and 0.125-0.5 additive genetic variance (VA). The results indicate that both methods performed well in alleviating the bias associated with ECP in all scenarios. The bias in VA estimates was reduced from 15-190% to 0-90% depending on the simulation parameters, structure and size of data sets. The second method outperformed the first in the cases of lower VA (.125) and/or higher ECP ratio (>30%). Estimates of the location parameters for ECP classes showed regular patterns. No changes in predicted breeding values were observed when ECP was considered. It is concluded that the proposed methods proved to be effective in addressing ECP.

Key Words: Binary Responses, Extreme Case Problem, Bayesian Approach

144 Analysis of binary responses in presence of extreme case problem classes. R. Rekaya, R. L. Sapp*, and J. K. Bertrand, *The University of Georgia*, *Athens*.

A simulation was carried out to investigate methods of analyzing binary responses when extreme case problem (ECP) classes (all observations in a given class were zeros or ones) were present. A linear mixed model that included a fixed effect and random effects of sire and residual at the liability scale was used to generate binary data. Four simulation scenarios were conducted based on varying percentage of ECP: 1) 5% (5E); 2) 10% (10E); 3) 20% (20E); and 4) 30% (30E). A generalized prior (g-prior) with varying weight was used for the ECP classes: 1) 0% or no g-prior (NG); 2) 5% (5G); 3) 10% (10G); and 4) 15% (15G). Five replicates of each data set were generated and analyzed with all four g-priors. In all cases, a standard threshold model was used for analysis. Point estimates of sire variance obtained from 5E, 10E, 20E, and 30E using NG (flat prior for fixed effects) were, as expected, severely biased. Depending on the percentage of ECP, these estimates were over estimated by 68 to 148% when NG was used. When a g-prior was used, the bias was reduced and even eliminated depending on the percentage of ECP and the weight assigned to the g-prior. Using 15G, bias was completely eliminated independently of the percentage of ECP. For 10G, the bias was eliminated for data sets with 5E and 10E and significantly reduced for data sets with 20E and 30E. With 5G, bias persisted using all four data sets. Pearson correlations between true and estimated fixed effects for 5E, 10E, 20E, and 30E were the lowest when NG was used; further, the correlations were similar when 5G, 10G, or 15G was used for the varying percentage of ECP data. However, Pearson correlations increased dramatically for all levels of ECP when 5G, 10G, or 15G was included in the analysis to account for ECP. The results of this study suggest that when analyzing binary data with ECP, bias in the estimation of variance components could be eliminated, or at least significantly reduced, using a g-prior. Further work is being conducted to apply this methodology to a more realistic scenario (animal model and joint analysis of binary and continuous traits).

Key Words: Binary Response, Generalized Prior, Simulation

145 Investigation into a regression model for crossbred performance. T. Lewis*[1,2], J. Woolliams[2], and J. Wiseman[1], [1]*University of Nottingham*, *Loughborough, Leicestershire, UK*, [2]*Roslin Institute*, *Roslin, Midlothian, UK*.

Heterosis is often calculated using F1 and F2 crosses. Since pig breeding schemes produce many types of cross, is it possible to exploit such data to determine the sufficiency of various heterosis models? The aim of the study was to estimate

litter number born alive (NBA) of 9 different cross-bred classes of Large White (LW) and Pietran (Pt) pigs, to estimate classical heterosis and determine the presence of epistasis via recombination loss.

51,180 records of LW and Pt pure and crosses were taken from a database provided by JSR Genetics Plc. NBA estimates for 9 types of cross (pure LW & Pt, F1, and backcrosses 1, 2 & 3) were made using a full linear mixed model with parity, serve number, mating method (AI or natural) and type of cross as fixed effects. An alternative reduced model was fitted with LW fraction, heterosis and recombination loss included as covariates. The fitted values obtained from the reduced regression model were compared to cross type estimates from the factor model. The regression model was also run using an extended dataset including records from 95 animals of the same LW fraction but different cross types.

Regression co-efficients of heterosis, recombination loss and LW fraction on NBA; and NBA means (under LW fraction = 1) and estimated differences from the mean across all LW fractions are shown in the table.

Regression estimates indicate a significant heterotic effect on NBA. Recombination loss effects appear large, suggesting strong additive x additive epistatic effects but large standard errors mean they can only be determined as significantly different to zero using the extended data. The reduced regression model provided a similar pattern of responses to the full model.
NBA means and estimated differences

LW fraction	Factor	Regression	Extended
1	8.449	8.347	8.411
0.9375	0.249	-0.216	-0.280
0.875	-1.151	-0.340	-0.450
0.75	0.434	-0.317	-0.461
0.5	0.805	0.821	0.832
0.25	-0.808	-0.354	-0.480
0.125	-0.468	-0.396	-0.478
0.0625	-0.467	-0.281	-0.312
0	-0.056	-0.075	-0.038
Regression Estimates			
LW Fraction	-	0.075 (0.19)	0.038 (0.19)
Heterosis	-	1.717 (0.44)	1.701 (0.44)
Recombination Loss	-	-5.819 (3.09)	-7.014 (2.96)

Key Words: Heterosis, Litter Size, Pigs

146 Blup with SAS. Z. Zhang*, *Cornell University*, *Ithaca, NY*.

The SAS procedure Mixed and statistical models with genetic correlated random effect are intensively and independently used in biological research. The limitation factor for the joint application is the complexity to construct variance of genetic correlated random effect among individuals. A computer program LORG in the form of SAS macro is presented to facilitate the joint applications. The macro automatically constructs a SAS dataset that defines the variance structure of genetic correlated random effect. The SAS dataset can be imported by SAS procedure Mixed with the option of GDATA or LDATA. The macro is flexible enough to allow users to select type of pedigree to calculate probability of identity by decent and fit multiple traits and multiple genetic correlated random variables. The use of the macros is demonstrated through an illustrative example on simulated data.

Key Words: Mixed Model, SAS, Pedigree

Dairy Foods: Products and Processing

147 Development of cold resistant strains of bifidobacteria by natural selection. S. Ibrahim*, *North Carolina Agricultural and Technical State University*, *Greensboro*.

Recent studies have shown the health benefits associated with regular consumption of dairy food products containing bifidobacteria. Because they provide a very favorable growing environment, dairy products have been the preferred medium to reintroduce viable populations of bifidobacteria into the GI tract. To provide health benefits, bifidobacteria must remain viable in large numbers in the carrier food. Consequently, it is important to establish the survival and viability of these cultures when subjected to refrigerated storage. The objectives of this study were to investigate whether the survivability or resistance of bifidobacteria in cold storage could be improved by natural selection and to test a cold resistant strain for β-galactosidase activity and autoaggregation behavior. Twenty-nine different bifidobacteria cultures were propagated in TPY broth. Strains were transferred daily for 29 weeks into fresh TPY broth and incubated at 37C. Natural selection of the bacteria was achieved by making daily transfers of the cultures into fresh TPY and by lowering the growth temperature two degrees every week. Growth was monitored by measuring the optical density (O.D.) at 610nm. Results indicated that all 29 strains were able to grow at lower temperatures (<37 C) and achieve high cell density. However, only 10 of the strains were able to survive growth temperature below 20 C and maintain high cell density (O.D. > 0.90). Five strains were able to survive temperatures below 15 C and had high cell density (O.D. > 0.80). Two strains were able to grow at 7 C and reached high cell density (O.D. >0.80). The β-galactosidase activities of these strains were similar to the wild strains and showed a marked ability to autoaggregate in TPY. These results suggest that some strains of bifidobacteria are cold resistant and that their growth can be further improved through by a natural selection process that favors the growth of cold resistant bacteria. These findings further suggest that bifidobacteria can survive and thrive in limited time cold storage, which supports their use in dairy products as a health promoting probiotics.

Key Words: Cold Resistant, Bifidobacteria

148 A unique Japanese functional yogurt containing specific egg yolk immunoglobulin to suppress *Helicobacter pylori* in humans. A. M. Abdou*[1], K. Horie[1], N. Horie[1], Y. Kodama[2], Y. Hoshikawa[3], T. Yamane[4], A. Hansen[2], and M. Kim[1], [1]*Pharma Foods International Company, Ltd.*, *Kyoto, Japan*, [2]*Ghen Corporation*, *Gifu-City, Japan*, [3]*Glico Dairy Products Company, Ltd.*, *Tokyo, Japan*, [4]*Matsushita Memorial Hospital*, *Osaka, Japan*.

Health-conscious consumers increasingly looking for foods that promote good health and could reduce risk of diseases. Dairy products are excellent media to generate an array of products that fit into the current consumer demand. In particular; scientific and clinical evidence is mounting to corroborate the consumer perception of health from yogurt.